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• Koyama, Tanetoshi  
Toyota-shi, Aichi (JP)

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(74) Representative: Bühling, Gerhard, Dipl.-Chem. et al  
Patentanwaltsbüro  
Tiedtke-Bühling-Kinne & Partner  
Bavariaring 4  
D-80336 München (DE)

(71) Applicant: TOYOTA JIDOSHA KABUSHIKI KAISHA

Aichi-ken (JP)

(72) Inventors:

- Kolke, Ayumi  
Toyota-shi, Aichi (JP)
- Obata, Shusel  
Toyota-shi, Aichi (JP)
- Ogura, Kyozo  
Toyota-shi, Aichi (JP)

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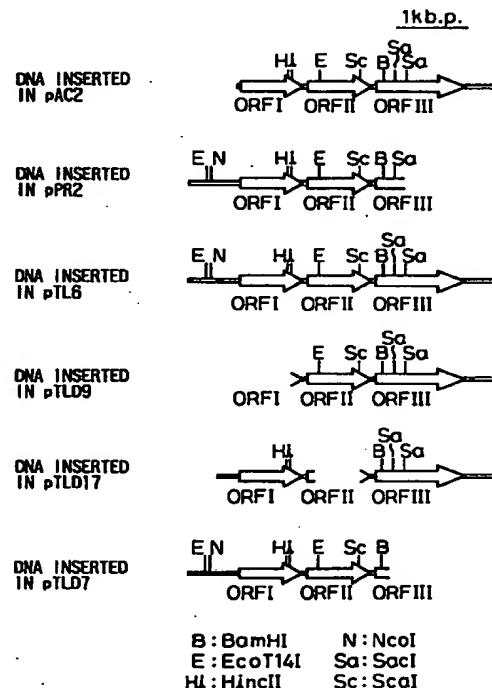
The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.

### (54) Heptaprenyl diphosphate synthesizing enzyme and DNA encoding same

(57) Heptaprenyl diphosphate (HDP)-synthetase derived from *Bacillus stearothermophilus* which enzymes have the amino acid sequences shown as SEQ ID NOs: 1 to 3; 1 and 2; 2 and 3; or 1 and 3, DNA encoding them, and a method of producing the enzymes.

According to the invention it is possible to industrially produce HDP-synthesizing enzyme and HPD.

Fig. 1



**Description****BACKGROUND OF INVENTION**5   **1. Field of Invention**

The present invention relates to heptaprenyl diphosphate (hereunder sometimes abbreviated to "HDP") synthetase of *Bacillus stearothermophilus* origin, to DNA encoding the enzyme, to an expression vector containing the DNA, to a host transformed by the expression vector, to a method of producing heptaprenyl diphosphate-synthesizing enzyme by 10 the host, and to a method of producing heptaprenyl diphosphate using the enzyme or host.

15   **2. Related Art**

HDP, synthesized from condensation reaction of 4 molecules of isopentenyl diphosphate and 1 molecule of farnesyl 20 diphosphate by HDP-synthetase, is an important biosynthetic intermediate of isoprenoids such as prenylquinone. Although HDP-synthetase, which is categorized into prenyl transferase, is known to be present in some microorganisms such as *Bacillus subtilis* (J. Biol. Chem. 255, p.4539-4543 (1980)), its amino acid sequence and the DNA sequence of the gene encoding it have not been known.

Genes coding for other prenyl transferase are known, farnesyl diphosphate synthetase ([2.5.1.1.] J. Biol. Chem. 25, p.4607-4614 (1990)), geranylgeranyl diphosphate synthetase (Proc. Natl. Acad. Sci. USA, 89, p.6761-6764). However, the tertiary structures of the known prenyl transferases are homodimers which comprise of two exactly same subunits, and it is different from the peculiar heterodimer of *Bacillus subtilis* HDP synthetase (FEBA Lett. 161, 257-260 (1983)). Therefore, absolutely no data exists regarding homology between the amino acid sequences of the former two and the latter.

Consequently, the present invention is aimed at providing HDP synthetase of *Bacillus stearothermophilus* origin, which was hitherto unknown in the species, DNA encoding the enzyme, and a method of production of the recombinant HDP synthetase using the DNA.

**SUMMARY OF INVENTION**

With the aim of accomplishing the above-mentioned object, the present inventors have been the first to succeed in cloning an HDP synthetase gene of *Bacillus stearothermophilus* origin, by the PCR method using synthesized primers designed from a portion of the known sequence of prenyl transferase, following hybridization using PCR amplified fragments as probe and measuring the expressed activity of the gene expression products.

Thus, the present invention provides a protein of *Bacillus stearothermophilus* origin having heptaprenyl diphosphate synthetase activity, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; a peptide with the amino acid sequence from the 1st amino acid Met to the 234th amino acid Arg of Sequence No. 2, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.

The present invention also provides a peptide of *Bacillus stearothermophilus* origin, which has the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.

The present invention further provides a peptide of *Bacillus stearothermophilus* origin, which has the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.

The present invention further provides a protein of *Bacillus stearothermophilus* origin with heptaprenyl diphosphate synthetase activity, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.

The present invention further provides a protein of *Bacillus stearothermophilus* origin with heptaprenyl diphosphate synthetase activity, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid

Met to the 234th amino acid Arg of Sequence No. 2, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.

The present invention further provides a protein of *Bacillus stearothermophilus* origin with heptaprenyl diphosphate synthetase activity, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 234th amino acid Arg of Sequence No. 2, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.

The present invention further provides DNA encoding the above-mentioned protein and various peptides.

The present invention further provides an expression vector comprising the above-mentioned DNA.

The present invention further provides a host transformed by the above-mentioned expression vector.

The present invention further provides a method of producing heptaprenyl diphosphate synthetase which is characterized by culturing the above-mentioned host, and collecting heptaprenyl diphosphate synthetase from the cultured product.

The present invention further provides a method of producing heptaprenyl diphosphate which is characterized by culturing the above-mentioned transformant, and collecting heptaprenyl diphosphate from the cultured product.

The present invention further provides a method of producing heptaprenyl diphosphate which is characterized by reacting the above-mentioned enzyme with a substrate.

## 20 BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the positional relationships and restriction enzyme maps for plasmids pAC2, pPR2, pTL6, pTLD9, pTLD17 and pTLD7 of the present invention.

Fig. 2 is a thin layer radiochromatograms of the reaction mixture prepared by incubation of isopentenyl diphosphate and farnesyl diphosphate with expression product of a DNA fragment of the present invention.

## DETAILED DESCRIPTION

The open reading frame portions of nucleotide sequences of DNA cloned from *Bacillus stearothermophilus* which express heptaprenyl diphosphate synthetase activity are shown as SEQ ID NOs: 1 to 3. There are 3 open reading frames (ORF). The first open reading frame (ORFI) is assumed to begin at the ATG coding for the 1st amino acid Met of SEQ ID NO: 1 and to end with the GGG coding for the 220th Gly. However, it may possibly begin at the ATG coding for the 19th amino acid Met, the ATG coding for the 20th amino acid Met, or the ATG coding for the 22nd amino acid Met.

The second open reading frame (ORFII) is assumed to begin at the ATG coding for the 1st amino acid Met of SEQ ID NO: 2 and to end with the CGG coding for the 234th amino acid Arg. However, this ORFII may possibly begin at the ATG coding for the 23rd amino acid Met of the amino acid sequence. The third open reading frame (ORFIII) is assumed to begin at the GTG coding for the 1st amino acid Val of SEQ ID NO: 3, and to end with the TAT coding for the 323rd amino acid Tyr. However, this ORFIII may possibly begin at the ATG coding for the 4th amino acid Met or the ATG coding for the 9th amino acid Met.

In the DNA containing the cloned ORFI-III, the nucleotide AACG locates between the translation termination codon TAG at the 3' end of ORFI and the translation initiation codon ATG (Met) of ORFII, and the nucleotide GTTAAG locates between the translation termination codon TGA of ORFII and the translation initiation codon GTG (Val) of ORFIII.

The full-length DNA expression product had the strongest heptaprenyl diphosphate synthetase activity and the expression products of ORFI and ORFIII, ORFI and ORFII, and ORFII and ORFIII also showed heptaprenyl diphosphate synthetase activity. Consequently, according to one embodiment of the present invention, there are provided DNA comprising all of ORFI, ORFII and ORFIII, heptaprenyl diphosphate synthetase consisting of the peptide encoded thereby, and a method for its production.

The present invention also provides DNA containing ORFI and ORFIII but not containing ORFII in its complete form, a peptide having heptaprenyl diphosphate synthetase activity which is expressed by that DNA, and a method for its production. The present invention further provides DNA containing ORFI and ORFII, or ORFII and ORFIII but not containing any other ORF in its complete form, a peptide expressed thereby, and a method for its production.

Plant-derived enzymes sometimes differ in a few amino acids depending on the variety of plants from which they are derived, and often differ in a few amino acids by natural mutations. In addition, the native activity of an enzyme is sometimes maintained even upon artificial mutation on the amino acid sequence. Consequently, the present invention also encompasses, in addition to peptides having the amino acid sequences represented by SEQ ID NOs: 1 to 3, also peptides with amino acid sequences resulting from variations of the amino acid sequences represented by SEQ ID NOs: 1 to 3 by means of a substitution, deletion and/or addition of one or a few, for example 5 or 10, amino acids, providing that the peptides are still have the enzyme activity.

The present invention further provides DNA encoding a peptide mutated in the manner described above, as well as a method of producing the mutated peptide.

As will be explained in detail by way of the examples, the DNA of the present invention may be cloned from *Bacillus stearothermophilus*. Also, DNA containing any one of ORFI, ORFII and ORFIII, all three, or ORFI and ORFIII, ORFI and ORFII or ORFII and ORFIII, and not containing any other ORF in its complete form, may be obtained by cutting full-length DNA using restriction endonucleases which cut within, for example, other ORFs outside of the aimed ORF without cutting within the latter. Alternatively, DNA encoding a mutated peptide may be obtained by the site-specific mutagenesis using, for example, a mutagenic primer.

Furthermore, once the amino acid sequence of one peptide is determined, it is possible to define a proper nucleotide sequence coding therefor, which then allows chemical synthesis of the DNA by conventional DNA synthesis methods. Each individual ORF of the present invention is not especially long, and thus may be easily synthesized by a person skilled in the art by conventional DNA synthesis methods.

The present invention further provides expression vectors comprising the DNA as described above, hosts transformed by the expression vectors, and a method of producing the enzyme or peptides of the present invention using these hosts.

The expression vector includes an origin of replication, the expression regulating sequence, etc., which differ depending on the host. The host may be a prokaryotic organism, for example a bacterium such as an *E. coli*, or *Bacillus* such as *Bacillus subtilis*; a eukaryotic organism, for example yeast, a fungus an example of which is *S. cerevisiae* belonging to the genus *Saccharomyces*, or fungus an example of which is a mold such as *A. niger* or *A. oryzae* belonging to the genus *Aspergillus*; animal cells such as cultured silk worm cells or cultured higher animal cells, for example CHO cells. Plant cells may also be used as hosts.

According to the present invention, as will be shown in the examples, it is possible to produce heptaprenyl diphosphate synthase by culturing a host transformed with DNA of the present invention, which accumulates the enzyme in the culture, and recovering it. Also, according to the present invention, heptaprenyl diphosphate may also be produced by allowing HDP synthetase produced by the method of the present invention to react with isopentenyl diphosphate and allylic diphosphate such as farnesyl diphosphate acid as substrates.

Referring to the use of *E. coli* as a host for an example, there are known gene expression regulating mechanism in the process of transcription of mRNA from DNA, the process of translation of protein from mRNA, etc. As promoter sequences which regulate mRNA synthesis, there are known, in addition to naturally occurring sequences (for example, lac, trp, bla, lpp, P<sub>L</sub>, P<sub>R</sub>, ter, T3, T7, etc.), also mutants thereof (for example, lacUV5) and sequences obtained by artificially fusing natural promoter sequences (for example, tac, trc, etc.), and these may also be used according to the present invention.

As sequences capable of regulating ability to synthesize protein from mRNA, the importance of the ribosome-binding site (GAGG and similar sequences) and the distance to the initiation codon ATG is already known. It is also well known that terminator sequences which govern completion of transcription at the 3' end (for example, vectors including rrnBT<sub>1</sub>T<sub>2</sub>) are commercially available from Pharmacia Co.) affect the efficiency of protein synthesis in recombinants.

Vectors which may be used to prepare the recombinant vectors of the present invention may be commercially available ones, or they may be any of a variety of derived vectors, depending on the purpose. As examples there may be mentioned pBR322, pBR327, pKK223-3, pKK233-2, pTrc99, etc. which carry the pMB1-derived replicon; pUC18, pUC19, pUC118, pUC119, pHSG298, pHSG396, etc. which have been modified for increased number of copies; pACYC177, pACYC184, etc. which carry the p15A-derived replicon; and plasmids derived from pSC101, ColE1, R1 or F factor.

In addition to plasmids, gene introduction is also possible by way of virus vectors such as λ-phage and M13 phage, and transposons. For gene introduction to microorganisms other than *E. coli*, there is known gene introduction to the genus *Bacillus* by pUB110 (available from Sigma Co.) and pHY300PLK (available from Takara Shuzo). These vectors are described in Molecular Cloning (J. Sambrook, E.F. Fritsch, T. Maniatis, published by Cold Spring Harbor Laboratory Press), Cloning Vector (P.H. Pouwels, B.E. Enger/Valk, W.J. Brammar, published by Elsevier), and various company catalogs.

In particular, pTrc99 (available from Pharmacia Co.) is preferred as a vector including, in addition to the ampicillin resistance gene as a selective marker, P<sub>trc</sub> and lacI<sup>q</sup> as a promoter and controlling gene, the sequence AGGA as a ribosome-binding site, and rrnBT<sub>1</sub>T<sub>2</sub> as the terminator, and having an expression regulating function on the HDP-synthesizing enzyme gene.

The incorporation into these vectors of a DNA fragment coding for HDP synthetase and if necessary a DNA fragment with the function of expression regulation on the gene for the above-mentioned enzyme, may be accomplished by a known method using an appropriate restriction endonuclease and ligase. Specifically the method described below may be conveniently followed. pTL6 may be mentioned as a definite plasmid of the present invention prepared in this manner.

As microorganisms for the gene introduction by such recombinant vectors, there may be used *Escherichia coli*, as well as microorganisms belonging to the genus *Bacillus*. The transformation may also be carried out by a conventional method, for example the CaCl<sub>2</sub> method or protoplast method described in Molecular Cloning (J. Sambrook, E.F. Fritsch,

T. Maniatis, published by Cold Spring Harbor Laboratory Press) or DNA Cloning Vol.I-III (ed. by D.M. Glover, published by IRL PRESS), etc.

A representative transformant according to the present invention which may be obtained is pTL6/JM109.

When these transformants or recombinant microorganism cells are cultured in medium normally used for *E. coli*, heptaprenyl diphosphate synthase (HDP synthase) accumulates in the cells. The HDP in the cells may be recovered by physical treatment in the absence or presence of a cytidylyc enzyme for lysis and a conventional isolation and purification method of for enzymes.

Lysozyme is preferably used as the cytidylyc enzyme, and ultrasonic waves are preferably used for physical treatment. Most of the *E. coli*-derived protein may be removed as insoluble deposit by heating at about 55°C. For the isolation and purification of the enzyme, any or a combination of gel filtration, ion exchange, hydrophobic, reverse phase, affinity or other type of chromatography, or ultrafiltration may be available.

During the process of isolation and purification, a reagent to stabilize the desired enzyme may be combined with the treatment solution, for example, a reducing agent such as β-mercaptoethanol or dithiothreitol, protective agent against proteases, such as PMSF or BSA, or metal ion such as magnesium.

Since the above-mentioned HDP synthetase activity may be measured, for example, in the manner described hereunder, it is recommended that the isolation and purification of the enzyme be performed while confirming the activity of the enzyme using the assay reaction solution employed in f) in Example 1 hereunder.

## EXAMPLES

An example of a method of preparing a DNA sequence, plasmid and transformant according to the present invention will now be described, but the scope of the invention is in no way restricted to this example.

### Example 1

The experiment was carried out basically in accordance with Molecular Cloning, DNA Cloning and the Takara Shuzo Catalog, mentioned previously. Most of the enzymes used were purchased from Takara Shuzo. The *Bacillus stearothermophilus* used was the known bacterium stored at the American Type Culture Collection (ATCC). Strain ATCC 10149 was used for this experiment.

#### a) Preparation of chromosomal DNA of *Bacillus stearothermophilus*

Culturing was performed in LB medium (1% tryptone, 0.5% yeast extract, 1% NaCl) at 55°C, and the cells were collected. After suspension in a lysis buffer, lysozyme (chicken albumen-derived, product of Sigma Co.) was added to 10 mg/ml. After lysis, 1/10 volume of 1M Tris·HCl (pH 8.0), 1/10 volume of 10% SDS and 1/50 volume of 5 M NaCl were added. Proteinase K (product of Sigma Co.) was added to 10 mg/ml, and the mixture was heated to 50°C.

An equivalent of phenol was added and the mixture stirred and centrifuged to remove the protein. The supernatant was taken with a wide-mouthed pipette into a beaker, and after a 2.5-fold amount of ethanol was gently layered thereon the chromosomal DNA was wound up on a glass rod. After dissolution in TE (10 mM Tris·HCl (pH 8.0), 1 mM EDTA), the DNA was treated with RNaseA (product of Sigma Co.), Proteinase K and phenol, a 2.5-fold amount of ethanol was gently layered thereon and the chromosomal DNA was wound up on a glass rod. After washing with 70% ethanol, it was dissolved in TE and used in the following experiment.

#### b) Acquisition of pCR64

DNA primers P1 (Sequence No. 4), P2 (Sequence No. 5), P4 (Sequence No. 6), P6 (Sequence No. 7), P8 (Sequence No. 8), P9 (Sequence No. 9), P10 (Sequence No. 10), P11 (Sequence No. 11), P12 (Sequence No. 12) and P13 (Sequence No. 13) were prepared based on the heretofore known conserved regions of the amino acid sequence of prenyl transferase.

The chromosomal DNA was subjected to partial digestion with Sau3AI, and the PCR (polymerase chain reaction) was conducted with combinations of synthetic DNA P1 and P4, P1 and P6, P1 and P8, P2 and P4, P2 and P6, P2 and P8, P9 and P11, P9 and P4, P9 and P6, P9 and P8, P9 and P13, P1 and P11, P2 and P11, P12 and P4, P12 and P6, P12 and P8, P12 and P13, P1 and P13, P2 and P13, P10 and P4, P10 and P6, P10 and P8, and P10 and P13.

The PCR product of the P10 and P8 combination was linked with the HinclI digestion product of plasmid pUC118 (purchased from Takara Shuzo) using T4DNA ligase, and *E. coli*/JM109 was transformed. Plasmids were prepared by the alkali SDS method, and the DNA sequences of 27 clones were analyzed with an Applied Biosystems 373A fluorescent

DNA sequencer. One of the sequences was referred as pCR64.

Table 1

## (Composition of PCR reaction solution)

Template DNA	1 µg
10 x AmpliTaq Buffer	10 µl
dNTPs mixture solution (1.25 mM each)	16 µl
Primer 1	100 pmol
Primer 2	100 pmol
Taq polymerase adjusted to 100 µl with H <sub>2</sub> O	2 units
(PCR reaction conditions)	
94°C, 30 secs	
↓	
50°C, 30 secs	x 35 cycles
↓	
72°C, 1 min	
↓	
72°C, 7 mins	
↓	
4°C	

25

c) Cloning of surrounding region with pCR64 as probe

30 c-1) A DNA fragment consisting of an approximately 500 bp pCR64 digestion product by restriction endonucleases KpnI and HindIII was labelled with DIG using a DIG DNA labeling kit (purchased from BOEHRINGER MANNHEIM). The instructions in the kit manual were followed.

## c-2) Preparation of library

35 The chromosomal DNA was digested with restriction endonuclease AccI, and upon Southern hybridization using the probe from c-1), a band was detected in the position of about 3 kbp. Here, the DNA fragment of about 3 kbp was isolated by agarose gel electrophoresis and treated with T4DNA polymerase. These were linked with the SmaI digestion product of plasmid pUC18 using T4DNA ligase, and *E. coli* JM109 was transformed.

## c-3) Screening

40 The library prepared in c-2) was screened with the probe prepared in c-1). Detection was made using a DIG DNA detection kit (purchased from BOEHRINGER MANNHEIM) and plasmid pAC2 was obtained. The instructions in the kit manual were followed. DNA sequence of the inserted gene of about 2.5 kbp was analyzed with an Applied Biosystems 373A fluorescent sequencer.

d) Isolation of pPR2

45 The gene library of c-2) was subjected to PCR using a synthetic DNA primer P64-4 (Sequence No. 14) prepared based on the DNA sequence obtained in c-3) and M13 Primer RV (purchased from Takara Shuzo). The amplification product was inserted into pT7 Blue T-Vector (purchased from Novagen) to obtain pPR2.

## 50 e) Linking of pAC2 and pPR2

DNA fragments of about 1 kbp and 5 kbp as BamHI digestion products of pAC2 and pPR2, respectively, were ligated to obtain pTL6.

## 55 f) Measurement of isoprenoid synthetase activity

The *E. coli* JM105 transformed with pTL6 was cultured overnight in 50 ml of LB medium containing 50 µg/ml of ampicillin, and the cells were collected. These were suspended in 4 ml of lysis buffer and disrupted with ultrasonic waves. Heating was performed at 55°C for 1 hour to inactivate the *E. coli*-derived prenyl transferase, and the *E. coli*-derived

denatured protein was removed by centrifugation and the supernatant was used for the assay. The assay reaction mixture was allowed to react for 1 hour or 14 hours at 55°C. The reaction mixture was extracted with 1-butanol, and the radioactivity was measured using a liquid scintillation counter.

Table 2

(Composition of lysis buffer)	
Tris·HCl (pH 7.7)	50 mM
EDTA	1 mM
β-Mercaptoethanol	10 mM
PMSF	0.1 mM
(Composition of assay reaction solution (total volume: 1 ml))	
Tris·HCl (pH 8.5)	50 mM
MgCl <sub>2</sub>	25 mM
NH <sub>4</sub> Cl	50 mM
β-Mercaptoethanol	50 mM
(all-E)-farnesyl diphosphate	25 nmoles
[1- <sup>14</sup> C]Isopentenyl diphosphate (product of Amersham Col., corresponding to approx. 5.5 × 10 <sup>4</sup> dpm)	25 nmoles
Cell-free extract	500 µl

The 1-butanol extract obtained from the above-mentioned reaction of JM105 carrying pTL6 was hydrolyzed and analyzed by thin-layer chromatography (TLC). As a result, the produced isoprenoid was identified as heptaprenyl diphosphate, thus showing that pTL6 contains the gene for heptaprenyl diphosphate synthetase (Fig. 2). Furthermore, upon investigating the specificity to allylic substrate primers in the assay system described hereunder (Table 3), particular enzyme activity was found with (all-E) farnesyl diphosphate and (all-E) geranylgeranyl diphosphate, whereas dimethylallyl diphosphate, geranyl diphosphate, (2Z, 6E)-farnesyl diphosphate, (2Z, 6E, 10E) geranylgeranyl diphosphate and (2Z, 6E, 10E, 14E) farnesylgeranyl diphosphate were not satisfactory substrates (Table 4).

Table 3

(Composition of assay reaction solution (total volume: 1 ml))	
Tris·HCl (pH 8.5)	50 mM
MgCl <sub>2</sub>	25 mM
NH <sub>4</sub> Cl	50 mM
β-Mercaptoethanol	50 mM
Allylic substrate	2.5 nmoles
[1- <sup>14</sup> C]Isopentenyl diphosphate (product of Amersham Col., corresponding to approx. 1.1 × 10 <sup>5</sup> dpm)	0.92 nmoles
Cell-free extract	500 µl

Table 4

Substrate specificity of HDP synthetase derived from DNA sequence of the present invention	
Substrate	Enzyme activity (dpm)
Dimethylallyl diphosphate	324
Geranyl diphosphate	381
(all-E) Farnesyl diphosphate	4163
(2Z, 6E) Farnesyl diphosphate	323
(all-E) Geranylgeranyl diphosphate	1514
(2Z, 6E, 10E) Geranylgeranyl diphosphate	648
(all-E) Farnesylgeranyl diphosphate	728
(2Z, 6E, 10E, 14E) Farnesylgeranyl diphosphate	281

*E. coli* normally has no heptaprenyl transferase or prenyl transferase with activity at 55°C. *E. coli* transformed with pTL6 is able to synthesize heptaprenyl diphosphate. Also, the fact that the activity is present at 55°C indicates that the *Bacillus stearothermophilus*-derived prenyl transferase encoded by pTL6 is highly thermostable. This also shows that the recombinant is useful for producing stable heptaprenyl diphosphate.

#### g) Preparation of pTL6 deletion mutants and identification of HDP synthetase gene

pTL6 had a gene insert of about 3 kbp, which contained three ORFs. Upon cleavage of pTL6 with restriction endonuclease and preparation of plasmid pTLD9 by deletion of ORF1, plasmid pTLD17 by deletion of ORFII and plasmid pTLD7 by deletion of ORFIII, and measurement of the isoprenoid-synthetase activities, activity was found for pTL6, pTLD9 and pTLD17. 1-Butanol extracts of reaction products of pTL6 and pTLD17 were hydrolyzed and analyzed by TLC, and the produced isoprenoid was confirmed to be heptaprenyl diphosphate.

Table 5

HDP synthetase activities derived from DNA sequences of the present invention (Radioactivity of 1-butanol extracts expressed in dpm units)	
Cell-free extract solution	Enzyme activity (dpm)
<i>E. coli</i> JM105	0
<i>E. coli</i> JM105 / pT7Blue T-Vector	0
<i>E. coli</i> JM105 / pTL6	750
<i>E. coli</i> JM105 / pTLD9	16
<i>E. coli</i> JM105 / pTLD17	129(*)
<i>E. coli</i> JM105 / pTLD7	0

\* = 14 hour reaction

According to the present invention there are provided DNA sequences coding for heptaprenyl diphosphate synthetase enzyme of *Bacillus stearothermophilus* origin. Recombinant microorganisms, obtained by incorporating the DNA sequences into expression vectors which are then used to transform appropriate *E. coli* strains, produce safe substances with heptaprenyl diphosphate synthetase activity and heptaprenyl diphosphate.

This effect is achieved by preparing the above-mentioned DNA sequences from chromosomes of *Bacillus stearothermophilus*, which is not so far taught in scientific literature.

5

## SEQUENCE LISTINGS

Sequence No.: 1

Sequence length: 663

10 Sequence type: nucleic acid

Strandedness: double

Topology: linear

15 Molecule type: Genomic DNA

Original source:

Organism: *Bacillus stearothermophilus*

Sequence:

20 ATG CTC GAT GGC GCT TCA ACG GCG CCG AGT GAG GCG GAG CGG TGC ATC 45  
Met Leu Asp Gly Ala Ser Thr Ala Pro Ser Glu Ala Glu Arg Cys Ile

5 10 15

25 ATC GCC ATG ATG CTC ATG CAG ATC GCC CTT GAT ACC CAC GAT GAG GTG 90  
Ile Ala Met Met Leu Met Gln Ile Ala Leu Asp Thr His Asp Glu Val  
20 25 30

30 ACA GAT GAC GGC GGC GAC TTG CGG GCG CGG CAG CTT GTC GTC CTG GCC 135  
Thr Asp Asp Gly Gly Asp Leu Arg Ala Arg Gln Leu Val Val Leu Ala  
35 40 45

GGC GAC TTG TAC AGC GGG CTG TAC TAT GAG TTG TTG GCG CGT TCG GGC 180  
Gly Asp Leu Tyr Ser Gly Leu Tyr Tyr Glu Leu Leu Ala Arg Ser Gly  
50 55 60

40 GAA ACG GCG CTC ATC CGC TCG TTC GCC GAG GCG GTC CGC GAT ATT AAC 225  
Glu Thr Ala Leu Ile Arg Ser Phe Ala Glu Ala Val Arg Asp Ile Asn  
65 70 75 80

GAG CAA AAA GTG CGG CTT TAC GAA AAA AAA GTA GAG CGG ATC GAG TCG 270

Glu Gln Lys Val Arg Leu Tyr Glu Lys Lys Val Glu Arg Ile Glu Ser

85 90 95

45 TTG TTT GCG GCG GTC GGC ACG ATC GAA TCG GCG TTG CTT GTC AAG CTC 315  
Leu Phe Ala Ala Val Glu Thr Ile Glu Ser Ala Leu Leu Val Lys Leu  
100 105 110

50 GCC GAC CGC ATG GCG GCG CCG CAG TGG GGG CAG TTT GCC TAT TCG TAT 360  
Ala Asp Arg Met Ala Ala Pro Gln Trp Gly Gln Phe Ala Tyr Ser Tyr  
115 120 125

55

5            TTG CTG ATG CGG CGC CTG CTG CTC GAG CAG GAA GCG TTC ATC CGC ACG  405  
 Leu Leu Met Arg Arg Leu Leu Leu Glu Gln Glu Ala Phe Ile Arg Thr  
 130                 135                 140  
 10            GGA GCT TCG GTG CTC TTT GAG CAA ATG GCG CAA ATC GCG TTC CCG CGC  450  
 Gly Ala Ser Val Leu Phe Glu Gln Met Ala Gln Ile Ala Phe Pro Arg  
 145                 150                 155                 160  
 15            GCG GAA ACG TTG ACG AAA GAG CAA AAG CGG CAT TTG CTC CGC TTT TGC  495  
 Ala Glu Thr Leu Thr Lys Glu Gln Lys Arg His Leu Leu Arg Phe Cys  
 165                 170                 175  
 20            CGC CGC TAT ATC GAC GGC TGC CGG GAG GCG CTG TTT GCG GCG AAA CTG  540  
 Arg Arg Tyr Ile Asp Gly Cys Arg Glu Ala Leu Phe Ala Ala Lys Leu  
 180                 185                 190  
 25            CCG GTC AAC GGC CTG CTG CAG CTC CGC GTG GCC GTG CTT TCC GGC GGG  585  
 Pro Val Asn Gly Leu Leu Gln Leu Arg Val Ala Val Leu Ser Gly Gly  
 195                 200                 205  
 30            TTT CAA GCC ATC GCC AAA AAG ACG GTG GAA GAA GGG TAG                 630  
 Phe Gln Ala Ile Ala Lys Lys Thr Val Glu Glu Gly \*\*\*  
 210                 215                 220  
 35                 663

Sequence No.: 2  
 Sequence length: 705  
 35            Sequence type: nucleic acid  
 Strandedness: double  
 Topology: linear  
 40            Molecule type: Genomic DNA  
 Original source:  
 Organism: *Bacillus stearothermophilus*  
 Sequence:  
 45            ATG CGT CAA TCG AAA GAA GAG CGA GTC CAT CGC GTA TTT GAA AAC ATT  45  
 Met Arg Gln Ser Lys Glu Glu Arg Val His Arg Val Phe Glu Asn Ile  
 5                 10                 15  
 50            TCT GCG CAT TAT GAC CGG ATG AAC TCC GTC ATC AGC TTC CGC CGC CAC  90  
 Ser Ala His Tyr Asp Arg Met Asn Ser Val Ile Ser Phe Arg Arg His  
 20                 25                 30

5 TTG AAG TGG CGC AAA GAC GTG ATG CGG CGG ATG AAT GTG CAA AAA GGC 135  
 Leu Lys Trp Arg Lys Asp Val Met Arg Arg Met Asn Val Gln Lys Gly  
 35 40 45  
 10 AAA AAA GCG CTC GAT GTG TGC TGT GGG ACG GCT GAC TGG ACG ATC GCC 180  
 Lys Lys Ala Leu Asp Val Cys Cys Gly Thr Ala Asp Trp Thr Ile Ala  
 50 55 60  
 15 TTG GCG GAG GCG GTC GGT CCG GAA GGG AAA GTG TAC GGC CTT GAT TTC 225  
 Leu Ala Glu Ala Val Gly Pro Glu Gly Lys Val Tyr Gly Leu Asp Phe  
 65 70 75 80  
 AGC GAA AAC ATG CTG AAA GTC GGC GAA CAG AAG GTA AAA GCG CGC GGG 270  
 Ser Glu Asn Met Leu Lys Val Gly Glu Gln Lys Val Lys Ala Arg Gly  
 85 90 95  
 20 TTG CAT AAT GTG AAG CTC ATT CAC GGC AAT GCG ATG CAG CTG CCG TTT 315  
 Leu His Asn Val Lys Leu Ile His Gly Asn Ala Met Gln Leu Pro Phe  
 100 105 110  
 25 CCT GAC AAT TCG TTC GAT TAT GTG ACG ATC GGC TTC GGT TTG CGC AAC 360  
 Pro Asp Asn Ser Phe Asp Tyr Val Thr Ile Gly Phe Gly Leu Arg Asn  
 115 120 125  
 30 GTC CCT GAC TAT ATG ACC GTG CTT AAG GAA ATG CAC CGG GTG ACG AAG 405  
 Val Pro Asp Tyr Met Thr Val Leu Lys Glu Met His Arg Val Thr Lys  
 130 135 140  
 CCG GGC GGC ATA ACC GTC TGC CTG GAA ACG TCG CAG CCG ACG CTG TTC 450  
 35 Pro Gly Gly Ile Thr Val Cys Leu Glu Thr Ser Gln Pro Thr Leu Phe  
 145 150 155 160  
 GGG TTT CGC CAG CTT TAC TAT TTT TAC TTC CGG TTT ATT ATG CCG CTG 495  
 Gly Phe Arg Gln Leu Tyr Tyr Phe Tyr Phe Arg Phe Ile Met Pro Leu  
 40 165 170 175  
 TTT GGC AAG CTG CTG GCG AAA AGC TAT GAG GAG TAC TCG TGG CTG CAG 540  
 Phe Gly Lys Leu Leu Ala Lys Ser Tyr Glu Glu Tyr Ser Trp Leu Gln  
 45 180 185 190  
 GAA TCG GCG CGC GAG TTT CCG GGG CGG GAC GAG CTG GCC GAG ATG TTC 585  
 Glu Ser Ala Arg Glu Phe Pro Gly Arg Asp Glu Leu Ala Glu Met Phe  
 195 200 205  
 50 CGC GCC GCC GGT TTT GTC GAT GTC GAG GTC AAA CCG TAC ACG TTT GGC 630  
 Arg Ala Ala Gly Phe Val Asp Val Glu Val Lys Pro Tyr Thr Phe Gly  
 210 215 220

GTG GCG GCG ATG CAC TTG GGC TAT AAA CGG TGA 675  
 Val Ala Ala Met His Leu Gly Tyr Lys Arg \*\*\*  
 225 230  
 705  
 Sequence No.: 3  
 Sequence length: 972  
 Sequence type: nucleic acid  
 Strandedness: double  
 Topology: linear  
 Molecule type: Genomic DNA  
 Original source:  
 Organism: *Bacillus stearothermophilus*  
 Sequence:  
 GTG AAC AAC ATG AAG TTA AAG GCG ATG TAT TCG TTT TTA AGC GAT GAT 45  
 Val Asn Asn Met Lys Leu Lys Ala Met Tyr Ser Phe Leu Ser Asp Asp  
 5 10 15  
 TTA GCG GCG GTC GAA GAG GAG CTT GAG CGG GCG GTT CAG TCG GAA TAC 90  
 Leu Ala Ala Val Glu Glu Glu Leu Glu Arg Ala Val Gln Ser Glu Tyr  
 20 25 30  
 GGG CCG CTT GGG GAA GCG GCG CTC CAT CTG TTG CAG GCG GGC GGA AAG 135  
 Gly Pro Leu Gly Glu Ala Ala Leu His Leu Leu Gln Ala Gly Gly Lys  
 35 40 45  
 CGG ATC CGT CCC GTT TTT GTC TTG CTT GCC GCC CGC TTC GGC CAA TAT 180  
 Arg Ile Arg Pro Val Phe Val Leu Leu Ala Ala Arg Phe Gly Gln Tyr  
 50 55 60  
 GAC CTT GAG CGG ATG AAG CAT GTT GCC GTT GCG CTC GAG CTC ATT CAT 225  
 Asp Leu Glu Arg Met Lys His Val Ala Val Ala Leu Glu Leu Ile His  
 65 70 75 80  
 ATG GCT TCG CTC GTC CAC GAC GAT GTG ATC GAC GAC GCC GAT TTG CGC 270  
 Met Ala Ser Leu Val His Asp Asp Val Ile Asp Asp Ala Asp Leu Arg  
 85 90 95  
 CGC GGC CGG CCG ACG ATC AAG GCG AAA TGG AGC AAC CGG TTC GCC ATG 315  
 Arg Gly Arg Pro Thr Ile Lys Ala Lys Trp Ser Asn Arg Phe Ala Met  
 100 105 110

5 TAC ACA GCA GGG GAT TAT TTG TTT GCC CGC TCG CTC GAA CGG ATG GCG GAG 360  
 Tyr Thr Gly Asp Tyr Leu Phe Ala Arg Ser Leu Glu Arg Met Ala Glu  
 115 120 125  
 10 CTC GGC AAC CCG CGC GCC CAT CAA GTG TTG GCG AAA ACG ATC GTG GAA 405  
 Leu Gly Asn Pro Arg Ala His Gln Val Leu Ala Lys Thr Ile Val Glu  
 130 135 140  
 15 GTG TGC CGC GGG GAA ATT GAG CAA ATT AAA GAC AAG TAC CGG TTT GAT 450  
 Val Cys Arg Gly Glu Ile Glu Gln Ile Lys Asp Lys Tyr Arg Phe Asp  
 145 150 155 160  
 20 CAG CCG CTG CGC ACG TAT TTG CGG CGC ATC CGT CGG AAA ACG GCG CTG 495  
 Gln Pro Leu Arg Thr Tyr Leu Arg Arg Ile Arg Arg Lys Thr Ala Leu  
 165 170 175  
 25 CTC ATC GCC GCG AGC TGC CAG CTT GGC GCC CTC GCT GCC GGC GCG CCG 540  
 Leu Ile Ala Ala Ser Cys Gln Leu Gly Ala Leu Ala Ala Gly Ala Pro  
 180 185 190  
 30 GAG CCG ATT GTG AAG CGG CTG TAC TGG TTC GGC CAT TAT GTC GGC ATG 585  
 Glu Pro Ile Val Lys Arg Leu Tyr Trp Phe Gly His Tyr Val Gly Met  
 195 200 205  
 35 TCG TTT CAA ATT ACC GAC GAC ATT CTC GAT TTC ACT GGG ACG GAG GAA 630  
 Ser Phe Gln Ile Thr Asp Asp Ile Leu Asp Phe Thr Gly Thr Glu Glu  
 210 215 220  
 40 CAG CTC GGC AAA CCG GCC GGA AGC GAC TTG CTA CAA GGA AAC GTC ACC 675  
 Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Leu Gln Gly Asn Val Thr  
 225 230 235 240  
 45 CTT CCT GTG CTG TAT GCC TTG AGC GAT GAG CGG GTG AAG GCG GCC ATT 720  
 Leu Pro Val Leu Tyr Ala Leu Ser Asp Glu Arg Val Lys Ala Ala Ile  
 245 250 255  
 50 GCA GCT GTC GGT CCG GAA ACG GAC GTT GCG GAA ATG GCG GCG GTC ATT 765  
 Ala Ala Val Gly Pro Glu Thr Asp Val Ala Glu Met Ala Ala Val Ile  
 260 265 270  
 TCC GCC ATT AAG CGG ACG GAC GCC ATT GAG CGG TCG TAT GCG TTA AGC 810  
 Ser Ala Ile Lys Arg Thr Asp Ala Ile Glu Arg Ser Tyr Ala Leu Ser  
 275 280 285  
 55 GAC CGT TAC CTT GAC AAG GCG CTT CAC CTT CTT GAC GGA CTG CCG ATG 855  
 Asp Arg Tyr Leu Asp Lys Ala Leu His Leu Leu Asp Gly Leu Pro Met  
 290 295 300

5 AAT GAG GCG CGC GGC CTG TTG CGC GAC CTC GCC CTT TAC ATC GGG AAA 900  
Asn Glu Ala Arg Gly Leu Leu Arg Asp Leu Ala Leu Tyr Ile Gly Lys  
305 310 315 320  
AGG GAT TAT TAA 945  
Arg Asp Tyr \*\*\*  
10 972

15 Sequence No.: 4  
Sequence length: 30  
Sequence type: nucleic acid  
Strandedness: single  
Topology: linear  
Molecule type: Synthetic DNA  
20 Sequence:  
CTNATHCAYG AYGAYYTNCC NTCNATGGAC 30

25 Sequence No.: 5  
Sequence length: 24  
Sequence type: nucleic acid  
Strandedness: single  
Topology: linear  
Molecule type: Synthetic DNA  
30 Sequence:  
GAYAAYGAYG AYYTNMGNMG NGGC 24

35 Sequence No.: 6  
Sequence length: 27  
Sequence type: nucleic acid  
Strandedness: single  
Topology: linear  
Molecule type: Synthetic DNA  
40 Sequence:  
ATCRTCNCKD ATYTGRAANG CNARNCC 27

45 Sequence No.: 7  
Sequence length: 27  
Sequence type: nucleic acid  
Strandedness: single  
Topology: linear  
Molecule type: Synthetic DNA  
50 Sequence:  
55

ATCNARDATR TCRTCNCKDA TYTGAA

27

5 Sequence No.: 8  
Sequence length: 21  
Sequence type: nucleic acid  
Strandedness: single  
10 Topology: linear  
Molecule type: Synthetic DNA  
Sequence:  
15 GTCRCTNCCN ACNGGYTTNC C 21  
Sequence No.: 9  
Sequence length: 20  
Sequence type: nucleic acid  
20 Strandedness: single  
Topology: linear  
Molecule type: Synthetic DNA  
Sequence:  
25 YTNGARGCNG GNGGNAARMG 20  
Sequence No.: 10  
Sequence length: 20  
30 Sequence type:  
Strandedness: single  
Topology: linear  
Molecule type: Synthetic DNA  
Sequence:  
35 TAYWSNYTNA THCAYGAYGA 20  
Sequence No.: 11  
Sequence length: 21  
40 Sequence type:  
Strandedness: single  
Topology: linear  
Molecule type: Synthetic DNA  
Sequence:  
45 YTCCATRTCN GCNGCYTGNC C 21  
Sequence No.: 12  
Sequence length: 26  
50 Sequence type: nucleic acid  
Strandedness: single

55

5                   Topology: linear  
 Molecule type: Synthetic DNA  
 Sequence:

10                  YTNGARTAYA THCAYMGNCA YAARAC

26

10                  Sequence No.: 13  
 Sequence length: 18  
 Sequence type: nucleic acid  
 Strandedness: single  
 Topology: linear  
 Molecule type: Synthetic DNA  
 Sequence:

15                  DATRTCNARD ATRTCRTC

18

20                  Sequence No.: 14  
 Sequence length: 20  
 Sequence type: nucleic acid  
 Strandedness: single  
 Topology: linear  
 Molecule type: Synthetic DNA  
 Sequence:

25                  GATCACATCG TCGTGGACGA

20

30                  Heptaprenyl diphosphate (HDP)-synthetase derived  
 from *Bacillus stearothermophilus* which enzymes have the  
 35                 amino acid sequences shown as SEQ ID NOs: 1 to 3; 1 and  
 2 and 3; or 1 and 3, DNA encoding them, and a method  
 of producing the enzymes.

40                  According to the invention it is possible to  
 industrially produce HDP-synthesizing enzyme and HPD.

45

50

55



	ACA GAT GAC GGC GGC GAC TTG CGG CGG CAG CTT GTC GTC CTG GCC		144
5	Thr Asp Asp Gly Gly Asp Leu Arg Ala Arg Gln Leu Val Val Leu Ala		
	35 40 45		
	GGC GAC TTG TAC AGC GGG CTG TAC TAT GAG TTG TTG GCG CGT TCG GGC		192
10	Gly Asp Leu Tyr Ser Gly Leu Tyr Tyr Glu Leu Leu Ala Arg Ser Gly		
	50 55 60		
	GAA ACG GCG CTC ATC CGC TCG TTC GCC GAG GCG GTC CGC GAT ATT AAC		240
	Glu Thr Ala Leu Ile Arg Ser Phe Ala Glu Ala Val Arg Asp Ile Asn		
	65 70 75 80		
15	GAG CAA AAA GTG CGG CTT TAC GAA AAA AAA GTA GAG CGG ATC GAG TCG		288
	Glu Gln Lys Val Arg Leu Tyr Glu Lys Lys Val Glu Arg Ile Glu Ser		
	85 90 95		
20	TTG TTT GCG GCG GTC GGC ACG ATC GAA TCG GCG TTG CTT GTC AAG CTC		336
	Leu Phe Ala Ala Val Gly Thr Ile Glu Ser Ala Leu Leu Val Lys Leu		
	100 105 110		
	GCC GAC CGC ATG GCG GCG CCG CAG TGG GGG CAG TTT GCC TAT TCG TAT		384
25	Ala Asp Arg Met Ala Ala Pro Gln Trp Gly Gln Phe Ala Tyr Ser Tyr		
	115 120 125		
	TTG CTG ATG CGG CGC CTG CTG CTC GAG CAG GAA GCG TTC ATC CGC ACG		432
	Leu Leu Met Arg Arg Leu Leu Glu Gln Glu Ala Phe Ile Arg Thr		
	130 135 140		
30	GGA GCT TCG GTG CTC TTT GAG CAA ATG GCG CAA ATC GCG TTC CCG CGC		480
	Gly Ala Ser Val Leu Phe Glu Gln Met Ala Gln Ile Ala Phe Pro Arg		
	145 150 155 160		
35	GCG GAA ACG TTG ACG AAA GAG CAA AAG CGG CAT TTG CTC CGC TTT TGC		528
	Ala Glu Thr Leu Thr Lys Glu Gln Lys Arg His Leu Leu Arg Phe Cys		
	165 170 175		
40	CGC CGC TAT ATC GAC GGC TGC CGG GAG GCG CTG TTT GCG GCG AAA CTG		576
	Arg Arg Tyr Ile Asp Gly Cys Arg Glu Ala Leu Phe Ala Ala Lys Leu		
	180 185 190		
45	CCG GTC AAC GGC CTG CTG CAG CTC CGC GTG GCC GTG CTT TCC GGC GGG		624
	Pro Val Asn Gly Leu Leu Gln Leu Arg Val Ala Val Leu Ser Gly Gly		
	195 200 205		
	TTT CAA GCC ATC GCC AAA AAG ACG GTG GAA GAA GGG TAG		663
	Phe Gln Ala Ile Ala Lys Lys Thr Val Glu Glu Gly		
	210 215 220		
50			

(2) INFORMATION FOR SEQ ID NO: 2:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 220 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15 Met Leu Asp Gly Ala Ser Thr Ala Pro Ser Glu Ala Glu Arg Cys Ile  
15 1 5 10 15

Ile Ala Met Met Leu Met Gln Ile Ala Leu Asp Thr His Asp Glu Val  
20 25 30

20 Thr Asp Asp Gly Gly Asp Leu Arg Ala Arg Gln Leu Val Val Leu Ala  
35 40 45

Gly Asp Leu Tyr Ser Gly Leu Tyr Tyr Glu Leu Leu Ala Arg Ser Gly  
50 55 60

25 Glu Thr Ala Leu Ile Arg Ser Phe Ala Glu Ala Val Arg Asp Ile Asn  
65 70 75 80

Glu Gln Lys Val Arg Leu Tyr Glu Lys Lys Val Glu Arg Ile Glu Ser  
 30                    85                    90                    95

Leu Phe Ala Ala Val Gly Thr Ile Glu Ser Ala Leu Leu Val Lys Leu  
                  100                 105                 110

35 Ala Asp Arg Met Ala Ala Pro Gln Trp Gly Gln Phe Ala Tyr Ser Tyr  
115 120 125

Leu Leu Met Arg Arg Leu Leu Leu Glu Gln Glu Ala Phe Ile Arg Thr  
130 135 140

Gly Ala Ser Val Leu Phe Glu Gln Met Ala Gln Ile Ala Phe Pro Arg  
145 150 155 160

Ala Glu Thr Leu Thr Lys Glu Gln Lys Arg His Leu Leu Arg Phe Cys  
165 170 175

Arg Arg Tyr Ile Asp Gly Cys Arg Glu Ala Leu Phe Ala Ala Lys Leu  
180 185 190

50 Pro Val Asn Gly Leu Leu Gln Leu Arg Val Ala Val Leu Ser Gly Gly  
195 200 205

Phe Gln Ala Ile Ala Lys Lys Thr Val Glu Glu Gly .  
210 215 220

## (2) INFORMATION FOR SEQ ID NO: 3:

5                   (i) SEQUENCE CHARACTERISTICS:  
                   (A) LENGTH: 705 base pairs  
                   (B) TYPE: nucleic acid  
                   (C) STRANDEDNESS: double  
                   (D) TOPOLOGY: linear

10                  (ii) MOLECULE TYPE: DNA (genomic)

15                  (vi) ORIGINAL SOURCE:  
                   (A) ORGANISM: *Bacillus stearothermophilus*

20                  (ix) FEATURE:  
                   (A) NAME/KEY: CDS  
                   (B) LOCATION: 1..705

## 25                  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CGT CAA TCG AAA GAA GAG CGA GTC CAT CGC GTA TTT GAA AAC ATT	48
Met Arg Gln Ser Lys Glu Glu Arg Val His Arg Val Phe Glu Asn Ile	
1                 5                 10                 15	
TCT GCG CAT TAT GAC CGG ATG AAC TCC GTC ATC AGC TTC CGC CGC CAC	96
Ser Ala His Tyr Asp Arg Met Asn Ser Val Ile Ser Phe Arg Arg His	
20                 25                 30	
TTG AAG TGG CGC AAA GAC GTG ATG CGG CGG ATG AAT GTG CAA AAA GGC	144
Leu Lys Trp Arg Lys Asp Val Met Arg Arg Met Asn Val Gln Lys Gly	
35                 40                 45	
AAA AAA GCG CTC GAT GTG TGC TGT GGG ACG GCT GAC TGG ACG ATC GCC	192
Lys Lys Ala Leu Asp Val Cys Cys Gly Thr Ala Asp Trp Thr Ile Ala	
50                 55                 60	
TTG GCG GAG GCG GTC GGT CCG GAA GGG AAA GTG TAC GGC CTT GAT TTC	240
Leu Ala Glu Ala Val Gly Pro Glu Gly Lys Val Tyr Gly Leu Asp Phe	
65                 70                 75                 80	
AGC GAA AAC ATG CTG AAA GTC GGC GAA CAG AAG GTA AAA GCG CGC GGG	288
Ser Glu Asn Met Leu Lys Val Gly Glu Gln Lys Val Lys Ala Arg Gly	
85                 90                 95	
TTG CAT AAT GTG AAG CTC ATT CAC GGC AAT GCG ATG CAG CTG CCG TTT	336
Leu His Asn Val Lys Leu Ile His Gly Asn Ala Met Gln Leu Pro Phe	
100                 105                 110	
CCT GAC AAT TCG TTC GAT TAT GTG ACG ATC GGC TTC GGT TTG CGC AAC	384
Pro Asp Asn Ser Phe Asp Tyr Val Thr Ile Gly Phe Gly Leu Arg Asn	
115                 120                 125	
GTC CCT GAC TAT ATG ACC GTG CTT AAG GAA ATG CAC CGG GTG ACC AAG	432
Val Pro Asp Tyr Met Thr Val Leu Lys Glu Met His Arg Val Thr Lys	
130                 135                 140	

	CCG GGC GGC ATA ACC GTC TGC CTG GAA ACG TCG CAG CCG ACG CTG TTC	480
5	Pro Gly Gly Ile Thr Val Cys Leu Glu Thr Ser Gln Pro Thr Leu Phe	
	145 150 155 160	
	GGG TTT CGC CAG CCT TAC TAT TTT TAC TTC CGG TTT ATT ATG CCG CTG	528
	Gly Phe Arg Gln Leu Tyr Tyr Phe Tyr Phe Arg Phe Ile Met Pro Leu	
10	165 170 175	
	TTT GGC AAG CTG CTG GCG AAA AGC TAT GAG GAG TAC TCG TGG CTG CAG	576
	Phe Gly Lys Leu Leu Ala Lys Ser Tyr Glu Glu Tyr Ser Trp Leu Gln	
	180 185 190	
15	GAA TCG GCG CGC GAG TTT CCG GGG CGG GAC GAG CTG GCC GAG ATG TTC	624
	Glu Ser Ala Arg Glu Phe Pro Gly Arg Asp Glu Leu Ala Glu Met Phe	
	195 200 205	
20	CGC GCC GCC GGT TTT GTC GAT GTC GAG GTC AAA CCG TAC ACG TTT GGC	672
	Arg Ala Ala Gly Phe Val Asp Val Glu Val Lys Pro Tyr Thr Phe Gly	
	210 215 220	
	GTG GCG GCG ATG CAC TTG GGC TAT AAA CGG TGA	705
	Val Ala Ala Met His Leu Gly Tyr Lys Arg	
25	225 230 235	
30		
35		
40		
45		
50		
55		

## (2) INFORMATION FOR SEQ ID NO: 4:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## 10 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Arg Gln Ser Lys Glu Glu Arg Val His Arg Val Phe Glu Asn Ile  
 1 5 10 15

15 Ser Ala His Tyr Asp Arg Met Asn Ser Val Ile Ser Phe Arg Arg His  
 20 25 30

Leu Lys Trp Arg Lys Asp Val Met Arg Arg Met Asn Val Gln Lys Gly  
 20 35 40 45

Lys Lys Ala Leu Asp Val Cys Cys Gly Thr Ala Asp Trp Thr Ile Ala  
 50 55 60

25 Leu Ala Glu Ala Val Gly Pro Glu Gly Lys Val Tyr Gly Leu Asp Phe  
 65 70 75 80

Ser Glu Asn Met Leu Lys Val Gly Glu Gln Lys Val Lys Ala Arg Gly  
 85 90 95

30 Leu His Asn Val Lys Leu Ile His Gly Asn Ala Met Gln Leu Pro Phe  
 100 105 110

Pro Asp Asn Ser Phe Asp Tyr Val Thr Ile Gly Phe Gly Leu Arg Asn  
 115 120 125

35 Val Pro Asp Tyr Met Thr Val Leu Lys Glu Met His Arg Val Thr Lys  
 130 135 140

40 Pro Gly Gly Ile Thr Val Cys Leu Glu Thr Ser Gln Pro Thr Leu Phe  
 145 150 155 160

Gly Phe Arg Gln Leu Tyr Tyr Phe Tyr Phe Arg Phe Ile Met Pro Leu  
 165 170 175

45 Phe Gly Lys Leu Leu Ala Lys Ser Tyr Glu Glu Tyr Ser Trp Leu Gln  
 180 185 190

Glu Ser Ala Arg Glu Phe Pro Gly Arg Asp Glu Leu Ala Glu Met Phe  
 195 200 205

50 Arg Ala Ala Gly Phe Val Asp Val Glu Val Lys Pro Tyr Thr Phe Gly  
 210 215 220

Val Ala Ala Met His Leu Gly Tyr Lys Arg  
 225 230

55

## (2) INFORMATION FOR SEQ ID NO: 5:

5                   (i) SEQUENCE CHARACTERISTICS:  
                   (A) LENGTH: 972 base pairs  
                   (B) TYPE: nucleic acid  
                   (C) STRANDEDNESS: double  
                   (D) TOPOLOGY: linear

10                  (ii) MOLECULE TYPE: DNA (genomic)

15                  (vi) ORIGINAL SOURCE:  
                   (A) ORGANISM: *Bacillus stearothermophilus*

20                  (ix) FEATURE:  
                   (A) NAME/KEY: CDS  
                   (B) LOCATION: 1..972

25                  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GTG AAC AAC ATG AAG TTA AAG GCG ATG TAT TCG TTT TTA AGC GAT GAT Val Asn Asn Met Lys Leu Lys Ala Met Tyr Ser Phe Leu Ser Asp Asp 1                 5                 10                 15	48
TTA GCG GCG GTC GAA GAG GAG CTT GAG CGG GCG GTT CAG TCG GAA TAC Leu Ala Ala Val Glu Glu Leu Glu Arg Ala Val Gln Ser Glu Tyr 20                 25                 30	96
GGG CCG CTT GGG GAA GCG GCG CTC CAT CTG TTG CAG GCG GGC GGA AAG Gly Pro Leu Gly Ala Ala Leu His Leu Leu Gln Ala Gly Gly Lys 35                 40                 45	144
CGG ATC CGT CCC GTT TTT GTC TTG CTT GCC GCC CGC TTC GGC CAA TAT Arg Ile Arg Pro Val Phe Val Leu Leu Ala Ala Arg Phe Gly Gln Tyr 50                 55                 60	192
GAC CTT GAG CGG ATG AAG CAT GTT GCC GTT GCG CTC GAG CTC ATT CAT Asp Leu Glu Arg Met Lys His Val Ala Val Ala Leu Glu Leu Ile His 65                 70                 75                 80	240
ATG GCT TCG CTC GTC CAC GAC GAT GTG ATC GAC GAC GCC GAT TTG CGC Met Ala Ser Leu Val His Asp Asp Val Ile Asp Asp Ala Asp Leu Arg 85                 90                 95	288
CGC GGC CGG CCG ACG ATC AAG GCG AAA TGG AGC AAC CGG TTC GCC ATG Arg Gly Arg Pro Thr Ile Lys Ala Lys Trp Ser Asn Arg Phe Ala Met 100                 105                 110	336
TAC ACA GGG GAT TAT TTG TTT GCC CGC TCG CTC GAA CGG ATG GCG GAG Tyr Thr Gly Asp Tyr Leu Phe Ala Arg Ser Leu Glu Arg Met Ala Glu 115                 120                 125	384
CTC GGC AAC CCG CGC GCC CAT CAA GTG TTG GCG AAA ACG ATC GTG GAA Leu Gly Asn Pro Arg Ala His Gln Val Leu Ala Lys Thr Ile Val Glu 130                 135                 140	432

	GTG TGC CGC GGG GAA ATT GAG CAA ATT AAA GAC AAG TAC CGG TTT GAT		480
5	Val Cys Arg Gly Glu Ile Glu Gln Ile Lys Asp Lys Tyr Arg Phe Asp		
	145 150 155 160		
	CAG CCG CTG CGC ACG TAT TTG CGG CGC ATC CGT CGG AAA ACG GCG CTG		528
10	Gln Pro Leu Arg Thr Tyr Leu Arg Arg Ile Arg Arg Lys Thr Ala Leu		
	165 170 175		
	CTC ATC GCC GCG AGC TGC CAG CTT GGC GCC CTC GCT GCC GGC GCG CCG		576
15	Leu Ile Ala Ala Ser Cys Gln Leu Gly Ala Leu Ala Ala Gly Ala Pro		
	180 185 190		
	GAG CCG ATT GTG AAG CGG CTG TAC TGG TTC GGC CAT TAT GTC GGC ATG		624
20	Glu Pro Ile Val Lys Arg Leu Tyr Trp Phe Gly His Tyr Val Gly Met		
	195 200 205		
	TCG TTT CAA ATT ACC GAC GAC ATT CTC GAT TTC ACT GGG ACG GAG GAA		672
25	Ser Phe Gln Ile Thr Asp Asp Ile Leu Asp Phe Thr Gly Thr Glu Glu		
	210 215 220		
	CAG CTC GGC AAA CCG GCC GGA AGC GAC TTG CTA CAA GGA AAC GTC ACC		720
30	Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Leu Gln Gly Asn Val Thr		
	225 230 235 240		
	CTT CCT GTG CTG TAT GCC TTG AGC GAT GAG CGG GTG AAG GCG GCC ATT		768
35	Leu Pro Val Leu Tyr Ala Leu Ser Asp Glu Arg Val Lys Ala Ala Ile		
	245 250 255		
40	GCA GCT GTC GGT CCG GAA ACG GAC GTT GCG GAA ATG GCG GCG GTC ATT		816
	Ala Ala Val Gly Pro Glu Thr Asp Val Ala Glu Met Ala Ala Val Ile		
	260 265 270		
	TCC GCC ATT AAG CGG ACG GAC GCC ATT GAG CGG TCG TAT GCG TTA AGC		864
45	Ser Ala Ile Lys Arg Thr Asp Ala Ile Glu Arg Ser Tyr Ala Leu Ser		
	275 280 285		
	GAC CGT TAC CTT GAC AAG GCG CTT CAC CTT GAC GGA CTG CCG ATG		912
50	Asp Arg Tyr Leu Asp Lys Ala Leu His Leu Leu Asp Gly Leu Pro Met		
	290 295 300		
	AAT GAG GCG CGC GGC CTG TTG CGC GAC CTC GCC CTT TAC ATC GGG AAA		960
55	Asn Glu Ala Arg Gly Leu Leu Arg Asp Leu Ala Leu Tyr Ile Gly Lys		
	305 310 315 320		
	AGG GAT TAT TAA		972
	Arg Asp Tyr		

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Val Asn Asn Met Lys Leu Lys Ala Met Tyr Ser Phe Leu Ser Asp Asp  
1 5 10 15

Leu Ala Ala Val Glu Glu Glu Leu Glu Arg Ala Val Gln Ser Glu Tyr  
 20 25 30

Gly Pro Leu Gly Glu Ala Ala Leu His Leu Leu Gln Ala Gly Gly Lys  
35 40 45

Arg Ile Arg Pro Val Phe Val Leu Leu Ala Ala Arg Phe Gly Gln Tyr  
50 55 60

Asp Leu Glu Arg Met Lys His Val Ala Val Ala Leu Glu Leu Ile His  
65 70 75 80

Met Ala Ser Leu Val His Asp Asp Val Ile Asp Asp Ala Asp Leu Arg  
85 90 95

Arg Gly Arg Pro Thr Ile Lys Ala Lys Trp Ser Asn Arg Phe Ala Met  
100 105 110

Tyr Thr Gly Asp Tyr Leu Phe Ala Arg Ser Leu Glu Arg Met Ala Glu  
 115                    120                    125

Leu Gly Asn Pro Arg Ala His Gln Val Leu Ala Lys Thr Ile Val Glu  
130 135 140

Val Cys Arg Gly Glu Ile Glu Gln Ile Lys Asp Lys Tyr Arg Phe Asp  
145 150 155 160

Gln Pro Leu Arg Thr Tyr Leu Arg Arg Ile Arg Arg Lys Thr Ala Leu  
165 170 175

Leu Ile Ala Ala Ser Cys Gln Leu Gly Ala Leu Ala Ala Gly Ala Pro  
180 185 190

Glu Pro Ile Val Lys Arg Leu Tyr Trp Phe Gly His Tyr Val Gly Met  
195 200 - 205

Leu Pro Val Leu Tyr Ala Leu Ser Asp Glu Arg Val Lys Ala Ala Ile  
245 250 255

Ala Ala Val Gly Pro Glu Thr Asp Val Ala Glu Met Ala Ala Val Ile  
5 260 265 270

Ser Ala Ile Lys Arg Thr Asp Ala Ile Glu Arg Ser Tyr Ala Leu Ser  
275 280 285

10 Asp Arg Tyr Leu Asp Lys Ala Leu His Leu Leu Asp Gly Leu Pro Met  
290 295 300

Asn Glu Ala Arg Gly Leu Leu Arg Asp Leu Ala Leu Tyr Ile Gly Lys  
305 310 315 320

15 Arg Asp Tyr

20

25

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35

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45

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55

(2) INFORMATION FOR SEQ ID NO: 7:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

15 CTNATHCAYG AYGAYYTNC NTCNATGGAC

30

20

(2) INFORMATION FOR SEQ ID NO: 8:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

35 GAYAAYGAYG AYYTNMGNMG NGGC

24

40

(2) INFORMATION FOR SEQ ID NO: 9:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55 ATCRTCNCKD ATYTGRAANG CNARNCC

27

5 (2) INFORMATION FOR SEQ ID NO: 10:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

15 ATCNARDATR TCRTCNCKDA TYTGAA

27

20

(2) INFORMATION FOR SEQ ID NO: 11:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

35 GTCRCTNCCN ACNGGYTTNC C

21

40

(2) INFORMATION FOR SEQ ID NO: 12:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

55 YTNGARGCNG GNNGNAARMG

20

55

(2) INFORMATION FOR SEQ ID NO: 13:

- 5                   (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 20 base pairs  
                     (B) TYPE: nucleic acid  
                     (C) STRANDEDNESS: single  
                     (D) TOPOLOGY: linear
- 10                  (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15                  TAYWSNYTNA THCAYGAYGA

20

20

(2) INFORMATION FOR SEQ ID NO: 14:

- 25                  (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 21 base pairs  
                     (B) TYPE: nucleic acid  
                     (C) STRANDEDNESS: single  
                     (D) TOPOLOGY: linear

- 30                  (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

35                  YTCCATRTCN GCNGCYTGNC C

21

40

(2) INFORMATION FOR SEQ ID NO: 15:

- 45                  (i) SEQUENCE CHARACTERISTICS:  
                     (A) LENGTH: 26 base pairs  
                     (B) TYPE: nucleic acid  
                     (C) STRANDEDNESS: single  
                     (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (synthetic)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

55                  YTNGARTAYA THCAYMGNCA YAARAC

26

55

## (2) INFORMATION FOR SEQ ID NO: 16:

- 5           (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 18 base pairs  
               (B) TYPE: nucleic acid  
               (C) STRANDEDNESS: single  
               (D) TOPOLOGY: linear

10           (ii) MOLECULE TYPE: DNA (synthetic)

15           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

DATRTCNARD ATRTCRTC

18

20           (2) INFORMATION FOR SEQ ID NO: 17:

- 25           (i) SEQUENCE CHARACTERISTICS:  
               (A) LENGTH: 20 base pairs  
               (B) TYPE: nucleic acid  
               (C) STRANDEDNESS: single  
               (D) TOPOLOGY: linear

30           (ii) MOLECULE TYPE: DNA (synthetic)

35           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GATCACATCG TCGTGGACGA

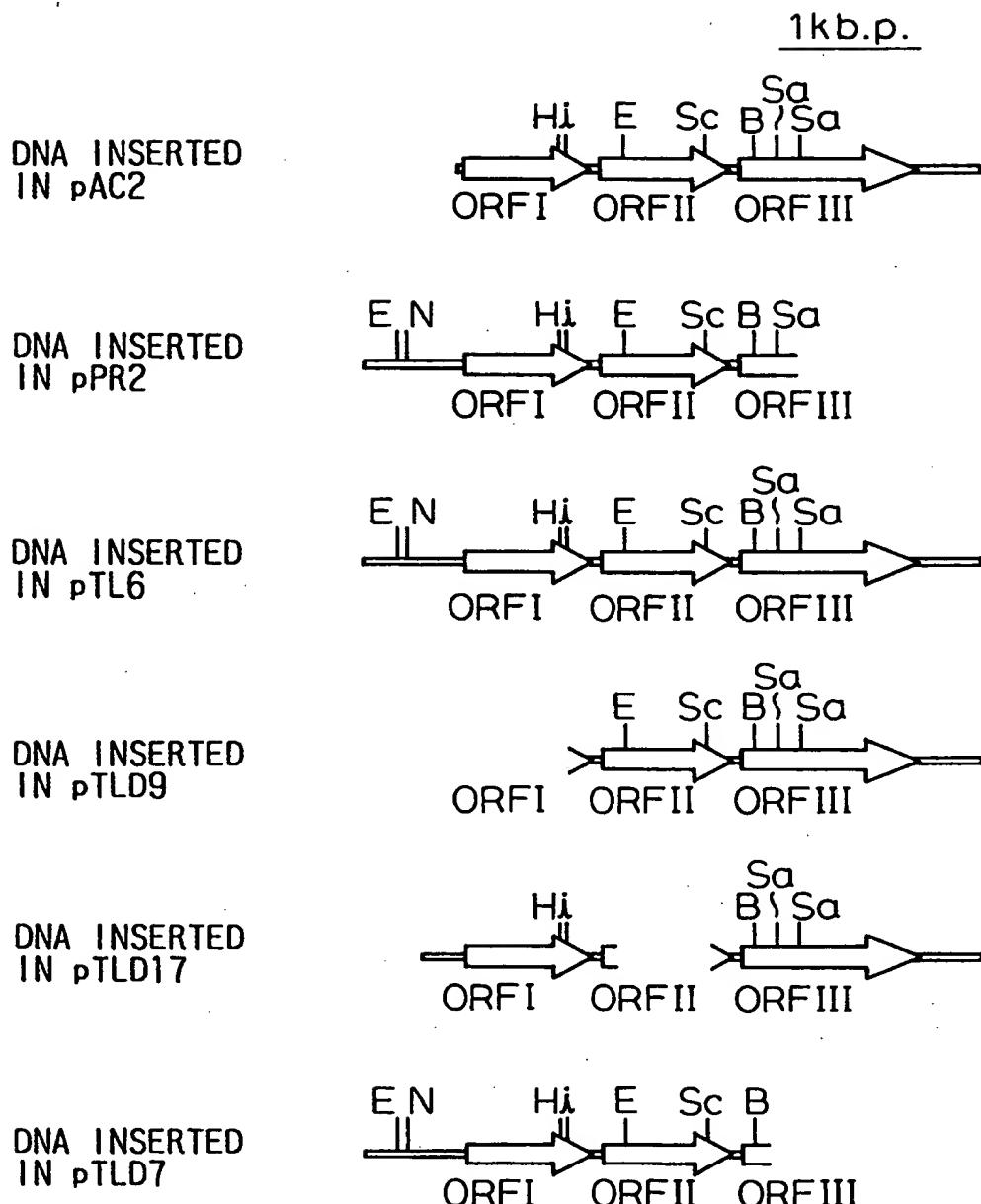
20

40           Claims

1. A protein of *Bacillus stearothermophilus* origin with heptaprenyl diphosphate synthetase activity, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; a peptide with the amino acid sequence from the 1st amino acid Met to the 234th amino acid Arg of Sequence No. 2, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.
2. A peptide of *Bacillus stearothermophilus* origin which has the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.
3. A peptide of *Bacillus stearothermophilus* origin, which has the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.

4. A protein of *Bacillus stearothermophilus* origin with heptaprenyl diphosphate synthetase activity, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.
- 5
5. A protein of *Bacillus stearothermophilus* origin, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 220th amino acid Gly of Sequence No. 1, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid Met to the 234th amino acid Arg of Sequence No. 2, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.
- 10
6. A protein of *Bacillus stearothermophilus* origin, which comprises a peptide with the amino acid sequence from the 1st amino acid Met to the 234th amino acid Arg of Sequence No. 2, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence; and a peptide with the amino acid sequence from the 1st amino acid Val to the 323rd amino acid Tyr of Sequence No. 3, or an amino acid sequence resulting from a substitution, deletion or addition of one or a few amino acids in the amino acid sequence.
- 15
- 20 7. DNA containing a base sequence encoding the 3 peptides according to Claim 1.
8. DNA encoding the peptide according to Claim 2.
9. DNA encoding the peptide according to Claim 3.
- 25
10. DNA encoding the two peptides according to Claim 4.
11. DNA encoding the two peptides according to Claim 5.
- 30
12. DNA encoding the two peptides according to Claim 6.
13. An expression vector comprising the DNA according to Claim 7.
- 35
14. A host transformed by the expression vector according to Claim 13.
15. The host according to Claim 14 which is a bacterium.
- 40
16. The host according to Claim 15 which is *Escherichia*.
- 45
17. A method of producing a peptide with heptaprenyl diphosphate synthetase activity or a related peptide, comprising the steps of culturing a host according to Claim 14, and recovering from the culture a peptide with heptaprenyl diphosphate synthetase activity or a related peptide.
18. A method of producing heptaprenyl diphosphate, comprising the steps of culturing a host according to Claim 14, and recovering heptaprenyl diphosphate from the culture.
- 50
19. A method of producing heptaprenyl diphosphate, comprising the steps of allowing the heptaprenyl diphosphate-synthesizing enzyme according to Claim 1, or a substance containing it, to act on an isopentenyl diphosphate, farnesyl diphosphate, geranylgeranyl diphosphate, farnesylgeranyl diphosphate or hexaprenyl diphosphate substrate.

Fig. 1



B : BamHI	N : NcoI
E : EcoT14I	Sa : SacI
Hi : HincII	Sc : ScaI

Fig.2

pTL6

